CLAIMS

1. Method for identifying biological species using samples of biological material deriving from a single species or a heterogeneous mixture of species and/or subspecies, characterised in that it comprises: (A) DNA extraction from the sample; (B) amplification of segments of the cytoplasmatic beta-actin gene by PCR or an equivalent technique; (C) identification of the amplified segment by comparison of its size in base pairs with a pre-established standard of sizes and/or identification of the amplified segment by DNA sequencing and comparison of the resulting sequence with the specific sequence of each species or subspecies present on a computer database.

2. Method according to claim 1, characterised in that in the amplification step using PCR or an equivalent technique, any segment of the cytoplasmatic beta-actin gene is amplified.

3. Method according to claim 2, characterised in that in the amplification step using PCR or an equivalent technique, gene segments of divergent regions of the cytoplasmatic beta-actin gene are amplified using DNA sequences with high evolutionary conservation between species and subspecies.

4. Method according to claim 2, characterised in that in the amplification step using PCR or an equivalent technique, the segments to be amplified are those which lie between the 3' sequence of the upstream exon and the 5' sequence of the downstream exon comprising the whole intronic sequence and part of the flanking exonic sequences.

5. Method according to claim 2, characterised in that the region or regions to be amplified are selected from the group consisting of the regions which lie between positions 1130-1473, 1452-2063, 2438-2680 and 2642-2960, numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277.

6. Method according to any of claims 1 to 5, characterised in that it uses a composition of universal primers that hybridise with the most highly conserved nucleotide regions of the cytoplasmatic beta-actin gene.

7. Method according to claim 6, characterised in that the universal primers hybridise with the sequences which lie between positions 1130-1191 and 1453-1473, numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277.

8. Method according to claim 6, characterised in that the universal primers hybridise with the sequences which lie between positions 1453-1473 and 2041-2065, numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277.

9. Method according to claim 6, characterised in that the universal primers hybridise with the sequences which lie between positions 2433-2459 and 2643-2680, numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277.

10. Method according to claim 6, characterised in that the universal primers hybridise with the sequences which lie between positions 2643-2680 and 2940-2960, numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277.

11. Method according to claim 6, characterised in that the universal primers are selected from the group consisting of: P1 (1132-1151) 5'TCCGGCATGTGCAAGGCCGG3', P2 (1474-1454) 5'CTCCATGTCGTCCCAGTTGG3', P3 (1453-1484) 5'ACCAACTGGGACGACATGGAGAAGATCTGGC3', P4 (2063-2034) 5'TACATGGCNGGGGTGTTAAAGGTCTCAAAC3', P5 (2434-2463) 5'TGCCCTGAGGCCCTCTTCCAGCCTTCCTTC3', P6 (2681-2643) 5'GGGTACATGGTGGTGCCGCCAGACAGCACNGTGTTGGC3', P7 (2643-2681) 5'GCCAACACNGTGCTGTCTGGCGGCACCACCATGTACCC3' and P8 (2952-2932) 5'TCGTACTCCTGCTTGCTGATCCACATCTG3'.

12. Method according to any of claims 1 to 11, characterised in that the samples are of biological origin.

13. Method according to claim 12, characterised in that the samples are taken from horse, goat, rabbit, dog, cat, chimpanzee, human and/or brown bear tissue.

14. Method according to any of claims 1 to 13, characterised in that in the identification step the amplified segment(s) is/are compared with the sequences of these same gene regions of species included on a computer database.

15. Use of DNA sequences of the cytoplasmatic beta-actin gene in biological samples deriving from a single species or from a heterogeneous mixture of species and/or subspecies, to identify the biological species to which the samples belong.